

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ihle, James N.
Silvennoinen, Ollie
Witthuhn, Bruce A.
Quelle, Frederick W.
- (ii) TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
Signal Transduction
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 - (B) STREET: 1100 New York Avenue, Suite 600
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: (To be assigned)
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fox, Samuel L.
 - (B) REGISTRATION NUMBER: 30,353
 - (C) REFERENCE/DOCKET NUMBER: 0656.0370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp	Ser	Xaa	Trp	Ser
1				5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Pro Glu Gly His Glu Tyr Tyr Arg Val Arg Glu Asp Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro
1 5 10 15

Ala Pro Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val
1 5 10 15

Thr Pro Ser

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg Leu Pro
 1 5 10 15
 Glu Pro Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3629 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 94..3480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGGGAACA AGATGTGAAC TGTTTTCCCT CCCAGAAGA AGAGGCCCTT TTTTCCCTC	60
CCGCGAAGGC CAATGTTCTG AAAAAAGCTC TAG ATG GGA ATG GCC TGC CTT ACA	114
Met Gly Met Ala Cys Leu Thr	
1 5	
ATG ACA GAA ATG GAG GCA ACC TCC ACA TCT CCT GTA CAT CAG AAT GGT	162
Met Thr Glu Met Glu Ala Thr Ser Thr Ser Pro Val His Gln Asn Gly	
10 15 20	
GAT ATT CCT GGA AGT GCT AAT TCT GTG AAG CAG ATA GAG CCA GTC CTT	210
Asp Ile Pro Gly Ser Ala Asn Ser Val Lys Gln Ile Glu Pro Val Leu	
25 30 35	
CAA GTG TAT CTG TAC CAT TCT CTT GGG CAA GCT GAA GGA GAG TAT CTG	258
Gln Val Tyr Leu Tyr His Ser Leu Gly Gln Ala Glu Gly Glu Tyr Leu	
40 45 50 55	
AAG TTT CCA AGT GGA GAG TAT GTT GCA GAA GAA ATT TGT GTG GCT GCT	306
Lys Phe Pro Ser Gly Glu Tyr Val Ala Glu Glu Ile Cys Val Ala Ala	
60 65 70	
TCT AAA GCT TGT GGT ATT ACG CCT GTG TAT CAT AAT ATG TTT GCG TTA	354
Ser Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu	
75 80 85	
ATG AGT GAA ACC GAA AGG ATC TGG TAC CCA CCC AAT CAT GTC TTC CAC	402
Met Ser Glu Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His	
90 95 100	
ATA GAC GAG TCA ACC AGG CAT GAC ATA CTC TAC AGG ATA AGG TTC TAC	450
Ile Asp Glu Ser Thr Arg His Asp Ile Leu Tyr Arg Ile Arg Phe Tyr	
105 110 115	
TTC CCT CAT TGG TAC TGT AGT GGC AGC AGC AGA ACC TAC AGA TAC GGA	498
Phe Pro His Trp Tyr Cys Ser Gly Ser Ser Arg Thr Tyr Arg Tyr Gly	
120 125 130 135	

GTG TCC CGT GGG GCT GAA GCT CCT CTG CTT GAT GAC TTT GTC ATG TCT Val Ser Arg Gly Ala Glu Ala Pro Leu Leu Asp Asp Phe Val Met Ser 140 145 150	546
TAC CTT TTT GCT CAG TGG CGG CAT GAT TTT GTT CAC GGA TGG ATA AAA Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val His Gly Trp Ile Lys 155 160 165	594
GTA CCT GTG ACT CAT GAA ACT CAG GAA GAG TGT CTT GGG ATG GCG GTG Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly Met Ala Val 170 175 180	642
TTA GAC ATG ATG AGA ATA GCT AAG GAG AAA GAC CAG ACT CCA CTG GCT Leu Asp Met Met Arg Ile Ala Lys Glu Lys Asp Gln Thr Pro Leu Ala 185 190 195	690
GTC TAT AAC TCT GTC AGC TAC AAG ACA TTC TTA CCA AAG TGC GTT CGA Val Tyr Asn Ser Val Ser Tyr Lys Thr Phe Leu Pro Lys Cys Val Arg 200 205 210 215	738
GCG AAG ATC CAA GAC TAT CAC ATT TTA ACC CGG AAG CGA ATC AGG TAC Ala Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr 220 225 230	786
AGA TTT CGC AGA TTC ATT CAG CAA TTC AGT CAA TGT AAA GCC ACT GCC Arg Phe Arg Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala 235 240 245	834
AGG AAC CTA AAA CTT AAG TAT CTT ATA AAC CTG GAA ACC CTG CAG TCT Arg Asn Leu Lys Leu Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser 250 255 260	882
GCC TTC TAC ACA GAA CAG TTT GAA GTA AAA GAA TCT GCA AGA GGT CCT Ala Phe Tyr Thr Glu Gln Phe Glu Val Lys Glu Ser Ala Arg Gly Pro 265 270 275	930
TCA GGT GAG GAG ATT TTT GCA ACC ATT ATA ATA ACT GGA AAC GGT GGA Ser Gly Glu Glu Ile Phe Ala Thr Ile Ile Ile Thr Gly Asn Gly Gly 280 285 290 295	978
ATT CAG TGG TCA AGA GGG AAA CAT AAG GAA AGT GAG ACA CTG ACA GAA Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser Glu Thr Leu Thr Glu 300 305 310	1026
CAG GAC GTA CAG TTA TAT TGT GAT TTC CCT GAT ATT ATT GAT GTC AGT Gln Asp Val Gln Leu Tyr Cys Asp Phe Pro Asp Ile Ile Asp Val Ser 315 320 325	1074
ATT AAG CAA GCA AAC CAG GAA TGC TCA AAT GAA AGT AGA ATT GTA ACT Ile Lys Gln Ala Asn Gln Glu Cys Ser Asn Glu Ser Arg Ile Val Thr 330 335 340	1122
GTC CAT AAA CAA GAT GGT AAA GTT TTG GAG ATA GAA CTT AGC TCA TTA Val His Lys Gln Asp Gly Lys Val Leu Glu Ile Glu Leu Ser Ser Leu 345 350 355	1170
AAA GAA GCC TTG TCA TTC GTG TCA TTA ATT GAC GGG TAT TAC AGA CTA Lys Glu Ala Leu Ser Phe Val Ser Leu Ile Asp Gly Tyr Tyr Arg Leu 360 365 370 375	1218
ACT GCG GAT GCG CAC CAT TAC CTC TGC AAA GAG GTG GCT CCC CCA GCT Thr Ala Asp Ala His His Tyr Leu Cys Lys Glu Val Ala Pro Pro Ala 380 385 390	1266
GTG CTC GAG AAC ATA CAC AGC AAC TGC CAC GGC CCA ATA TCA ATG GAT Val Leu Glu Asn Ile His Ser Asn Cys His Gly Pro Ile Ser Met Asp 395 400 405	1314

TTT GCC ATT AGC AAA CTA AAG AAG GCG GGT AAC CAG ACT GGA CTA TAT Phe Ala Ile Ser Lys Leu Lys Lys Ala Gly Asn Gln Thr Gly Leu Tyr 410 415 420	1362
GTG CTA CGA TGC AGC CCT AAG GAC TTC AAC AAA TAC TTT CTG ACC TTT Val Leu Arg Cys Ser Pro Lys Asp Phe Asn Lys Tyr Phe Leu Thr Phe 425 430 435	1410
GCT GTT GAG CGA GAA AAT GTC ATT GAA TAT AAA CAC TGT TTG ATT ACG Ala Val Glu Arg Glu Asn Val Ile Glu Tyr Lys His Cys Leu Ile Thr 440 445 450 455	1458
AAG AAT GAG AAT GGA GAA TAC AAC CTC AGC GGG ACT AAG AGG AAC TTC Lys Asn Glu Asn Gly Glu Tyr Asn Leu Ser Gly Thr Lys Arg Asn Phe 460 465 470	1506
AGT AAC CTT AAG GAC CTT TTG AAT TGC TAC CAG ATG GAA ACT GTG CGC Ser Asn Leu Lys Asp Leu Leu Asn Cys Tyr Gln Met Glu Thr Val Arg 475 480 485	1554
TCA GAC AGT ATC ATC TTC CAG TTT ACC AAA TGC TGC CCC CCA AAG CCA Ser Asp Ser Ile Ile Phe Gln Phe Thr Lys Cys Cys Pro Pro Lys Pro 490 495 500	1602
AAA GAT AAA TCA AAC CTT CTC GTC TTC AGA ACA AAT GGT ATT TCT GAT Lys Asp Lys Ser Asn Leu Leu Val Phe Arg Thr Asn Gly Ile Ser Asp 505 510 515	1650
GTT CAG ATC TCA CCA ACA TTA CAG AGG CAT AAT AAT GTG AAT CAA ATG Val Gln Ile Ser Pro Thr Leu Gln Arg His Asn Asn Val Asn Gln Met 520 525 530 535	1698
GTG TTT CAC AAA ATC AGG AAT GAA GAT TTA ATA TTT AAT GAA AGT CTT Val Phe His Lys Ile Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu 540 545 550	1746
GGC CAA GGT ACT TTT ACA AAA ATT TTT AAA GGT GTA AGA AGA GAA GTT Gly Gln Gly Thr Phe Thr Lys Ile Phe Lys Gly Val Arg Arg Glu Val 555 560 565	1794
GGA GAT TAT GGT CAA CTG CAC AAA ACG GAA GTT CTT TTG AAA GTC CTA Gly Asp Tyr Gly Gln Leu His Lys Thr Glu Val Leu Lys Val Leu 570 575 580	1842
GAT AAA GCA CAT AGG AAC TAT TCA GAG TCT TTC TTC GAA GCA GCA AGC Asp Lys Ala His Arg Asn Tyr Ser Glu Ser Phe Phe Glu Ala Ala Ser 585 590 595	1890
ATG ATG AGT CAG CTT TCT CAC AAG CAT TTG GTT TTG AAT TAT GGT GTC Met Met Ser Gln Leu Ser His Lys His Leu Val Leu Asn Tyr Gly Val 600 605 610 615	1938
TGT GTC TGT GGA GAG GAG AAC ATT CTG GTT CAA GAA TTT GTA AAA TTT Cys Val Cys Gly Glu Glu Asn Ile Leu Val Gln Glu Phe Val Lys Phe 620 625 630	1986
GGA TCA CTG GAT ACA TAC CTG AAG AAG AAC AAA AAT TCC ATA AAT ATA Gly Ser Leu Asp Thr Tyr Leu Lys Lys Asn Lys Asn Ser Ile Asn Ile 635 640 645	2034
TTA TGG AAA CTT GGA GTG GCT AAG CAG TTG GCA TGG GCC ATG CAT TTT Leu Trp Lys Leu Gly Val Ala Lys Gln Leu Ala Trp Ala Met His Phe 650 655 660	2082

CTA GAA GAA AAA TCC CTT ATT CAT GGG AAT GTG TGT GCT AAA AAT ATC Leu Glu Glu Lys Ser Leu Ile His Gly Asn Val Cys Ala Lys Asn Ile 665 670 675	2130
CTG CTT ATC AGA GAA GAA GAC AGG AGA ACG GGG AAC CCA CCT TTC ATC Leu Leu Ile Arg Glu Glu Asp Arg Arg Thr Gly Asn Pro Pro Phe Ile 680 685 690 695	2178
AAA CTT AGT GAT CCT GGC ATT AGC ATT ACA GTT CTA CCG AAG GAC ATT Lys Leu Ser Asp Pro Gly Ile Ser Ile Thr Val Leu Pro Lys Asp Ile 700 705 710	2226
CTT CAG GAG AGA ATA CCA TGG GTA CCT CCT GAA TGC ATT GAG AAT CCT Leu Gln Glu Ile Pro Trp Val Pro Pro Glu Cys Ile Glu Asn Pro 715 720 725	2274
AAA AAT CTC AAT CTG GCA ACA GAC AAG TGG AGC TTC GGG ACC ACT CTG Lys Asn Leu Asn Leu Ala Thr Asp Lys Trp Ser Phe Gly Thr Thr Leu 730 735 740	2322
TGG GAG ATC TGC AGT GGA GGA GAT AAG CCC CTG AGT GCT CTG GAT TCT Trp Glu Ile Cys Ser Gly Gly Asp Lys Pro Leu Ser Ala Leu Asp Ser 745 750 755	2370
CAA AGA AAG CTG CAG TTC TAT GAA GAT AAG CAT CAG CTT CCT GCA CCC Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro Ala Pro 760 765 770 775	2418
AAG TGG ACA GAG TTA GCA AAC CTT ATA AAT AAT TGC ATG GAC TAT GAG Lys Trp Thr Glu Leu Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu 780 785 790	2466
CCA GAT TTC AGG CCT GCT TTC AGA GCT GTC ATC CGT GAT CTT AAC AGC Pro Asp Phe Arg Pro Ala Phe Arg Ala Val Ile Arg Asp Leu Asn Ser 795 800 805	2514
CTG TTT ACT CCA GAT TAT GAA CTA CTA ACA GAA AAT GAC ATG CTA CCA Leu Phe Thr Pro Asp Tyr Glu Leu Leu Thr Glu Asn Asp Met Leu Pro 810 815 820	2562
AAC ATG AGA ATA GGT GCC CTA GGG TTT TCT GGT GCT TTT GAA GAC AGG Asn Met Arg Ile Gly Ala Leu Gly Phe Ser Gly Ala Phe Glu Asp Arg 825 830 835	2610
GAC CCT ACA CAG TTT GAA GAG AGA CAC TTG AAG TTT CTA CAG CAG CTT Asp Pro Thr Gln Phe Glu Glu Arg His Leu Lys Phe Leu Gln Gln Leu 840 845 850 855	2658
GGC AAA GGT AAC TTC GGG AGT GTG GAG ATG TGC CGC TAT GAC CCG CTG Gly Lys Gly Asn Phe Gly Ser Val Glu Met Cys Arg Tyr Asp Pro Leu 860 865 870	2706
CAG GAC AAC ACT GGC GAG GTG GTC GCT GTG AAG AAA CTC CAG CAC AGC Gln Asp Asn Thr Gly Glu Val Val Ala Val Lys Lys Leu Gln His Ser 875 880 885	2754
ACT GAA GAG CAC CTC CGA GAC TTT GAG AGG GAG ATC GAG ATC CTG AAA Thr Glu Glu His Leu Arg Asp Phe Glu Arg Glu Ile Glu Ile Leu Lys 890 895 900	2802
TCC TTG CAG CAT GAC AAC ATC GTC AAG TAC AAG GGA GTG TGC TAC AGT Ser Leu Gln His Asp Asn Ile Val Lys Tyr Lys Gly Val Cys Tyr Ser 905 910 915	2850
GCG GGT CGG CGC AAC CTA AGA TTA ATT ATG GAA TAT TTA CCA TAT GGA Ala Gly Arg Arg Asn Leu Arg Leu Ile Met Glu Tyr Leu Pro Tyr Gly 920 925 930 935	2898

AGT TTA CGA GAC TAT CTC CAA AAA CAT AAA GAA CGG ATA GAT CAC AAA Ser Leu Arg Asp Tyr Leu Gln Lys His Lys Glu Arg Ile Asp His Lys 940 945 950	2946
AAA CTT CTT CAA TAC ACA TCT CAG ATA TGC AAG GGC ATG GAA TAT CTT Lys Leu Leu Gln Tyr Thr Ser Gln Ile Cys Lys Gly Met Glu Tyr Leu 955 960 965	2994
GGT ACA AAA AGG TAT ATC CAC AGG GAC CTG GCA ACA AGG AAC ATA TTG Gly Thr 970 Arg Tyr Ile His Arg Asp Leu Ala Thr Arg Asn Ile Leu 975 980	3042
GTG GAA AAT GAG AAC AGG GTT AAA ATA GGA GAC TTC GGA TTA ACC AAA Val Glu Asn Glu Asn Arg Val Lys Ile Gly Asp Phe Gly Leu Thr Lys 985 990 995	3090
GTC TTG CCG CAG GAC AAA GAA TAC TAC AAA GTA AAG GAG CCA GGG GAA Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly Glu 1000 1005 1010 1015	3138
AGC CCC ATA TTC TGG TAC GCA CCT GAA TCC TTG ACG GAG AGC AAG TTT Ser Pro Ile Phe Trp Tyr Ala Pro Glu Ser Leu Thr Glu Ser Lys Phe 1020 1025 1030	3186
TCT GTG GCC TCA GAT GTG TGG AGC TTT GGA GTG GTT CTA TAC GAA CTT Ser Val Ala Ser Asp Val Trp Ser Phe Gly Val Val Leu Tyr Glu Leu 1035 1040 1045	3234
TTC ACA TAC ATC GAG AAG AGT AAA AGT CCA CCC GTG GAA TTT ATG CGA Phe Thr Tyr Ile Glu Lys Ser Lys Ser Pro Pro Val Glu Phe Met Arg 1050 1055 1060	3282
ATG ATT GGC AAT GAT AAA CAA GGG CAA ATG ATT GTG TTC CAT TTG ATA Met Ile Gly Asn Asp Lys Gln Gly Gln Met Ile Val Phe His Leu Ile 1065 1070 1075	3330
GAG CTA CTG AAG AGC AAC GGA AGA TTG CCA AGG CCA GAA GGA TGC CCA Glu Leu Leu Lys Ser Asn Gly Arg Leu Pro Arg Pro Glu Gly Cys Pro 1080 1085 1090 1095	3378
GAT GAG ATT TAT GTG ATC ATG ACA GAG TGC TGG AAC AAC AAT GTG AGC Asp Glu Ile Tyr Val Ile Met Thr Glu Cys Trp Asn Asn Asn Val Ser 1100 1105 1110	3426
CAG CGT CCC TCC TTC AGG GAC CTT TCG TTC GGG TGG ATC AAA TCC GGG Gln Arg Pro Ser Phe Arg Asp Leu Ser Phe Gly Trp Ile Lys Ser Gly 1115 1120 1125	3474
ACA GTA TAGCTGCGTG AAAGAGATGG CCTTCACTCA GAGACCAAGC AGACTTCCAG Thr Val	3530
AACCAGAACAA AAGCTCTGTA GCCTTGTGTC TACACATCCT TATCATGATG CTAGCTAGGC	3590
AGAAGAAACT GTGACGCCGT CTGCTCAAAG CTTTGCTTC	3629

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Ala Thr Ser Thr
1 5 10 15
Ser Pro Val His Gln Asn Gly Asp Ile Pro Gly Ser Ala Asn Ser Val
20 25 30
Lys Gln Ile Glu Pro Val Leu Gln Val Tyr Leu Tyr His Ser Leu Gly
35 40 45
Gln Ala Glu Gly Glu Tyr Leu Lys Phe Pro Ser Gly Glu Tyr Val Ala
50 55 60
Glu Glu Ile Cys Val Ala Ala Ser Lys Ala Cys Gly Ile Thr Pro Val
65 70 75 80
Tyr His Asn Met Phe Ala Leu Met Ser Glu Thr Glu Arg Ile Trp Tyr
85 90 95
Pro Pro Asn His Val Phe His Ile Asp Glu Ser Thr Arg His Asp Ile
100 105 110
Leu Tyr Arg Ile Arg Phe Tyr Phe Pro His Trp Tyr Cys Ser Gly Ser
115 120 125
Ser Arg Thr Tyr Arg Tyr Gly Val Ser Arg Gly Ala Glu Ala Pro Leu
130 135 140
Leu Asp Asp Phe Val Met Ser Tyr Leu Phe Ala Gln Trp Arg His Asp
145 150 155 160
Phe Val His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu
165 170 175
Glu Cys Leu Gly Met Ala Val Leu Asp Met Met Arg Ile Ala Lys Glu
180 185 190
Lys Asp Gln Thr Pro Leu Ala Val Tyr Asn Ser Val Ser Tyr Lys Thr
195 200 205
Phe Leu Pro Lys Cys Val Arg Ala Lys Ile Gln Asp Tyr His Ile Leu
210 215 220
Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg Arg Phe Ile Gln Gln Phe
225 230 235 240
Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu Lys Tyr Leu Ile
245 250 255
Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Gln Phe Glu Val
260 265 270
Lys Glu Ser Ala Arg Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile
275 280 285
Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys
290 295 300
Glu Ser Glu Thr Leu Thr Glu Gln Asp Val Gln Leu Tyr Cys Asp Phe
305 310 315 320
Pro Asp Ile Ile Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Cys Ser
325 330 335
Asn Glu Ser Arg Ile Val Thr Val His Lys Gln Asp Gly Lys Val Leu
340 345 350

Glu Ile Glu Leu Ser Ser Leu Lys Glu Ala Leu Ser Phe Val Ser Leu
 355 360 365
 Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys
 370 375 380
 Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile His Ser Asn Cys
 385 390 395 400
 His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys Lys Ala
 405 410 415
 Gly Asn Gln Thr Gly Leu Tyr Val Leu Arg Cys Ser Pro Lys Asp Phe
 420 425 430
 Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu
 435 440 445
 Tyr Lys His Cys Leu Ile Thr Lys Asn Glu Asn Gly Glu Tyr Asn Leu
 450 455 460
 Ser Gly Thr Lys Arg Asn Phe Ser Asn Leu Lys Asp Leu Leu Asn Cys
 465 470 475 480
 Tyr Gln Met Glu Thr Val Arg Ser Asp Ser Ile Ile Phe Gln Phe Thr
 485 490 495
 Lys Cys Cys Pro Pro Lys Pro Lys Asp Lys Ser Asn Leu Leu Val Phe
 500 505 510
 Arg Thr Asn Gly Ile Ser Asp Val Gln Ile Ser Pro Thr Leu Gln Arg
 515 520 525
 His Asn Asn Val Asn Gln Met Val Phe His Lys Ile Arg Asn Glu Asp
 530 535 540
 Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys Ile Phe
 545 550 555 560
 Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Lys Thr
 565 570 575
 Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu
 580 585 590
 Ser Phe Phe Glu Ala Ala Ser Met Met Ser Gln Leu Ser His Lys His
 595 600 605
 Leu Val Leu Asn Tyr Gly Val Cys Val Cys Gly Glu Glu Asn Ile Leu
 610 615 620
 Val Gln Glu Phe Val Lys Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys
 625 630 635 640
 Asn Lys Asn Ser Ile Asn Ile Leu Trp Lys Leu Gly Val Ala Lys Gln
 645 650 655
 Leu Ala Trp Ala Met His Phe Leu Glu Glu Lys Ser Leu Ile His Gly
 660 665 670
 Asn Val Cys Ala Lys Asn Ile Leu Leu Ile Arg Glu Glu Asp Arg Arg
 675 680 685
 Thr Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Ser Ile
 690 695 700

Thr Val Leu Pro Lys Asp Ile Leu Gln Glu Arg Ile Pro Trp Val Pro
705 710 715 720

Pro Glu Cys Ile Glu Asn Pro Lys Asn Leu Asn Leu Ala Thr Asp Lys
725 730 735

Trp Ser Phe Gly Thr Thr Leu Trp Glu Ile Cys Ser Gly Gly Asp Lys
740 745 750

Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp
755 760 765

Lys His Gln Leu Pro Ala Pro Lys Trp Thr Glu Leu Ala Asn Leu Ile
770 775 780

Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg Pro Ala Phe Arg Ala
785 790 795 800

Val Ile Arg Asp Leu Asn Ser Leu Phe Thr Pro Asp Tyr Glu Leu Leu
805 810 815

Thr Glu Asn Asp Met Leu Pro Asn Met Arg Ile Gly Ala Leu Gly Phe
820 825 830

Ser Gly Ala Phe Glu Asp Arg Asp Pro Thr Gln Phe Glu Glu Arg His
835 840 845

Leu Lys Phe Leu Gln Gln Leu Gly Lys Gly Asn Phe Gly Ser Val Glu
850 855 860

Met Cys Arg Tyr Asp Pro Leu Gln Asp Asn Thr Gly Glu Val Val Ala
865 870 875 880

Val Lys Lys Leu Gln His Ser Thr Glu Glu His Leu Arg Asp Phe Glu
885 890 895

Arg Glu Ile Glu Ile Leu Lys Ser Leu Gln His Asp Asn Ile Val Lys
900 905 910

Tyr Lys Gly Val Cys Tyr Ser Ala Gly Arg Arg Asn Leu Arg Leu Ile
915 920 925

Met Glu Tyr Leu Pro Tyr Gly Ser Leu Arg Asp Tyr Leu Gln Lys His
930 935 940

Lys Glu Arg Ile Asp His Lys Lys Leu Leu Gln Tyr Thr Ser Gln Ile
945 950 955 960

Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr Ile His Arg Asp
965 970 975

Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn Arg Val Lys Ile
980 985 990

Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp Lys Glu Tyr Tyr
995 1000 1005

Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp Tyr Ala Pro Glu
1010 1015 1020

Ser Leu Thr Glu Ser Lys Phe Ser Val Ala Ser Asp Val Trp Ser Phe
1025 1030 1035 1040

Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Ile Glu Lys Ser Lys Ser
1045 1050 1055

Pro Pro Val Glu Phe Met Arg Met Ile Gly Asn Asp Lys Gln Gly Gln
 1060 1065 1070
 Met Ile Val Phe His Leu Ile Glu Leu Leu Lys Ser Asn Gly Arg Leu
 1075 1080 1085
 Pro Arg Pro Glu Gly Cys Pro Asp Glu Ile Tyr Val Ile Met Thr Glu
 1090 1095 1100
 Cys Trp Asn Asn Asn Val Ser Gln Arg Pro Ser Phe Arg Asp Leu Ser
 1105 1110 1115 1120
 Phe Gly Trp Ile Lys Ser Gly Thr Val
 1125

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3429 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GCT TTC TGT GCT AAA ATG AGG AGC TCC AAG AAG ACT GAG GTG AAC Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn 1 5 10 15	48
CTG GAG GCC CCT GAG CCA GGG GTG GAA GTG ATC TTC TAT CTG TCG GAC Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp 20 25 30	96
AGG GAG CCC CTC CGG CTG GGC AGT GGA GAG TAC ACA GCA GAG GAA CTG Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu 35 40 45	144
TGC ATC AGG GCT GCA CAG GCA TGC CGT ATC TCT CCT CTT TGT CAC AAC Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn 50 55 60	192
CTC TTT GCC CTG TAT GAC GAG AAC ACC AAG CTC TGG TAT GCT CCA AAT Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn 65 70 75 80	240
CGC ACC ATC ACC GTT GAT GAC AAG ATG TCC CTC CGG CTC CAC TAC CGG Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg 85 90 95	288
ATG AGG TTC TAT TTC ACC AAT TGG CAT GGA ACC AAC GAC AAT GAG CAG Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln 100 105 110	336
TCA GTG TGG CGT CAT TCT CCA AAG AAG CAG AAA AAT GGC TAC GAG AAA Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys 115 120 125	384
AAA AAG ATT CCA GAT GCA ACC CCT CTC CTT GAT GCC AGC TCA CTG GAG Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu 130 135 140	432

TAT CTG TTT GCT CAG GGA CAG TAT GAT TTG GTG AAA TGC CTG GCT CCT Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro 145 150 155 160	480
ATT CGA GAC CCC AAG ACC GAG CAG GAT GGA CAT GAT ATT GAG AAC GAG Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu 165 170 175	528
TGT CTA GGG ATG GCT GTC CTG GCC ATC TCA CAC TAT GCC ATG ATG AAG Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys 180 185 190	576
AAG ATG CAG TTG CCA GAA CTG CCC AAG GAC ATC AGC TAC AAG CGA TAT Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr 195 200 205	624
ATT CCA GAA ACA TTG AAT AAG TCC ATC AGA CAG AGG AAC CTT CTC ACC Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr 210 215 220	672
AGG ATG CGG ATA AAT AAT GTT TTC AAG GAT TTC CTA AAG GAA TTT AAC Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn 225 230 235 240	720
AAC AAG ACC ATT TGT GAC AGC AGC GTG TCC ACG CAT GAC CTG AAG GTG Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val 245 250 255	768
AAA TAC TTG GCT ACC TTG GAA ACT TTG ACA AAA CAT TAC GGT GCT GAA Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu 260 265 270	816
ATA TTT GAG ACT TCC ATG TTA CTG ATT TCA TCA GAA AAT GAG ATG AAT Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn 275 280 285	864
TGG TTT CAT TCG AAT GAC GGT GGA AAC GTT CTC TAC TAC GAA GTG ATG Trp Phe His Ser Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met 290 295 300	912
GTG ACT GGG AAT CTT GGA ATC CAG TGG AGG CAT AAA CCA AAT GTT GTT Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val 305 310 315 320	960
TCT GTT GAA AAG GAA AAA AAT AAA CTG AAG CGG AAA AAA CTG GAA AAT Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn 325 330 335	1008
AAA GAC AAG AAG GAT GAG GAG AAA AAC AAG ATC CGG GAA GAG TGG AAC Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn 340 345 350	1056
AAT TTT TCA TTC TTC CCT GAA ATC ACT CAC ATT GTA ATA AAG GAG TCT Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser 355 360 365	1104
GTG GTC AGC ATT AAC AAG CAG GAC AAC AAG AAA ATG GAA CTG AAG CTC Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu 370 375 380	1152
TCT TCC CAC GAG GAG GCC TTG TCC TTT GTG TCC CTG GTA GAT GGC TAC Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr 385 390 395 400	1200
TTC CGG CTC ACA GCA GAT GCC CAT CAT TAC CTC TGC ACC GAC GTG GCC Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala 405 410 415	1248

CCC CCG TTG ATC GTC CAC AAC ATA CAG AAT GGC TGT CAT GGT CCA ATC Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile 420 425 430	1296
TGT ACA GAA TAC GCC ATC AAT AAA TTG CGG CAA GAA GGA AGC GAG GAG Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu 435 440 445	1344
GGG ATG TAC GTG CTG AGG TGG AGC TGC ACC GAC TTT GAC AAC ATC CTC Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu 450 455 460	1392
ATG ACC GTC ACC TGC TTT GAG AAG TCT GAG CAG GTG CAG GGT GCC CAG Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln 465 470 475 480	1440
AAG CAG TTC AAG AAC TTT CAG ATC GAG GTG CAG AAG GGC CGC TAC AGT Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser 485 490 495	1488
CTG CAC GGT TCG GAC CGC AGC TTC CCC AGC TTG GGA GAC CTC ATG AGC Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser 500 505 510	1536
CAC CTC AAG AAG CAG ATC CTG CGC ACG GAT AAC ATC AGC TTC ATG CTA His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu 515 520 525	1584
AAA CGC TGC TGC CAG CCC AAG CCC CGA GAA ATC TCC AAC CTG CTG GTG Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val 530 535 540	1632
GCT ACT AAG AAA GCC CAG GAG TGG CAG CCC GTC TAC CCC ATG AGC CAG Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln 545 550 555 560	1680
CTG AGT TTC GAT CGG ATC CTC AAG AAG GAT CTG GTG CAG GGC GAG CAC Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His 565 570 575	1728
CTT GGG AGA GGC ACG AGA ACA CAC ATC TAT TCT GGG ACC CTG ATG GAT Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp 580 585 590	1776
TAC AAG GAT GAC GAA GGA ACT TCT GAA GAG AAG AAG ATA AAA GTG ATC Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile 595 600 605	1824
CTC AAA GTC TTA GAC CCC AGC CAC AGG GAT ATT TCC CTG GCC TTC TTC Leu Lys Val Leu Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe 610 615 620	1872
GAG GCA GCC AGC ATG ATG AGA CAG GTC TCC CAC AAA CAC ATC GTG TAC Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr 625 630 635 640	1920
CTC TAT GGC GTC TGT GTC CGC GAC GTG GAG AAT ATC ATG GTG GAA GAG Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu 645 650 655	1968
TTT GTG GAA GGG GGT CCT CTG GAT CTC TTC ATG CAC CGG AAA AGT GAT Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp 660 665 670	2016
GTC CTT ACC ACA CCA TGG AAA TTC AAA GTT GCC AAA CAG CTG GCC AGT Val Leu Thr Thr Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser 675 680 685	2064

GCC CTG AGC TAC TTG GAG GAT AAA GAC CTG GTC CAT GGA AAT GTG TGT Ala Leu Ser Tyr Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys 690 695 700	2112
ACT AAA AAC CTC CTC CTG GCC CGT GAG GGA ATC GAC AGT GAG TGT GGC Thr Lys Asn Leu Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly 705 710 715 720	2160
CCA TTC ATC AAG CTC AGT GAC CCC GGC ATC CCC ATT ACG GTG CTG TCT Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser 725 730 735	2208
AGG CAA GAA TGC ATT GAA CGA ATC CCA TGG ATT GCT CCT GAG TGT GTT Arg Gln Glu Cys Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val 740 745 750	2256
GAG GAC TCC AAG AAC CTG AGT GTG GCT GCT GAC AAG TGG AGC TTT GGA Glu Asp Ser Lys Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly 755 760 765	2304
ACC ACG CTC TGG GAA ATC TGC TAC AAT GGC GAG ATC CCC TTG AAA GAC Thr Thr Leu Trp Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp 770 775 780	2352
AAG ACG CTG ATT GAG AAA GAG AGA TTC TAT GAA AGC CGG TGC AGG CCA Lys Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro 785 790 795 800	2400
GTG ACA CCA TCA TGT AAG GAG CTG GCT GAC CTC ATG ACC CGC TGC ATG Val Thr Pro Ser Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met 805 810 815	2448
AAC TAT GAC CCC AAT CAG AGG CCT TTC TTC CGA GCC ATC ATG AGA GAC Asn Tyr Asp Pro Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp 820 825 830	2496
ATT AAT AAG CTT GAA GAG CAG AAT CCA GAT ATT GTT TCC AGA AAA AAA Ile Asn Lys Leu Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys 835 840 845	2544
AAC CAG CCA ACT GAA GTG GAC CCC ACA CAT TTT GAG AAG CGC TTC CTA Asn Gln Pro Thr Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu 850 855 860	2592
AAG AGG ATC CGT GAC TTG GGA GAG GGC CAC TTT GGG AAG GTT GAG CTC Lys Arg Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu 865 870 875 880	2640
TGC AGG TAT GAC CCC GAA GAC AAT ACA GGG GAG CAG GTG GCT GTT AAA Cys Arg Tyr Asp Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys 885 890 895	2688
TCT CTG AAG CCT GAG AGT GGA GGT AAC CAC ATA GCT GAT CTG AAA AAG Ser Leu Lys Pro Glu Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys 900 905 910	2736
GAA ATC GAG ATC TTA AGG AAC CTC TAT CAT GAG AAC ATT GTG AAG TAC Glu Ile Glu Ile Leu Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr 915 920 925	2784
AAA GGA ATC TGC ACA GAA GAC GGA GGA AAT GGT ATT AAG CTC ATC ATG Lys Gly Ile Cys Thr Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met 930 935 940	2832
GAA TTT CTG CCT TCG GGA AGC CTT AAG GAA TAT CTT CCA AAG AAT AAG Glu Phe Leu Pro Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys 945 950 955 960	2880

AAC AAA ATA AAC CTC AAA CAG CAG CTA AAA TAT GCC GTT CAG ATT TGT Asn Lys Ile Asn Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys 965 970 975	2928
AAG GGG ATG GAC TAT TTG GGT TCT CGG CAA TAC GTT CAC CGG GAC TTG Lys Gly Met Asp Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu 980 985 990	2976
GCA GCA AGA AAT GTC CTT GTT GAG AGT GAA CAC CAA GTG AAA ATT GGA Ala Ala Arg Asn Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly 995 1000 1005	3024
GAC TTC GGT TTA ACC AAA GCA ATT GAA ACC GAT AAG GAG TAT TAC ACC Asp Phe Gly Leu Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr 1010 1015 1020	3072
GTC AAG GAT GAC CGG GAC AGC CCT GTG TTT TGG TAT GCT CCA GAA TGT Val Lys Asp Asp Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys 1025 1030 1035 1040	3120
TTA ATG CAA TCT AAA TTT TAT ATT GCC TCT GAC GTC TGG TCT TTT GGA Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly 1045 1050 1055	3168
GTC ACT CTG CAT GAG CTG CTG ACT TAC TGT GAT TCA GAT TCT AGT CCC Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro 1060 1065 1070	3216
ATG GCT TTG TTC CTG AAA ATG ATA GGC CCA ACC CAT GGC CAG ATG ACA Met Ala Leu Phe Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr 1075 1080 1085	3264
GTC ACA AGA CTT GTG AAT ACG TTA AAA GAA GGA AAA CGC CTG CCG TGC Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys 1090 1095 1100	3312
CCA CCT AAC TGT CCA GAT GAG GTT TAT CAG CTT ATG AGA AAA TGC TGG Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp 1105 1110 1115 1120	3360
GAA TTC CAA CCA TCC AAT CGG ACA AGC TTT CAG AAC CTT ATT GAA GGA Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly 1125 1130 1135	3408
TTT GAA GCA CTT TTA AAA TAA Phe Glu Ala Leu Lys 1140	3429

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Phe	Cys	Ala	Lys	Met	Arg	Ser	Ser	Lys	Lys	Thr	Glu	Val	Asn
1				5						10				15	
Leu	Glu	Ala	Pro	Glu	Pro	Gly	Val	Glu	Val	Ile	Phe	Tyr	Leu	Ser	Asp
			20					25					30		

Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu
35 40 45

Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn
50 55 60

Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn
65 70 75 80

Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg
85 90 95

Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln
100 105 110

Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys
115 120 125

Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu
130 135 140

Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro
145 150 155 160

Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu
165 170 175

Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys
180 185 190

Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr
195 200 205

Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr
210 215 220

Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn
225 230 235 240

Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val
245 250 255

Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu
260 265 270

Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn
275 280 285

Trp Phe His Ser Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met
290 295 300

Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val
305 310 315 320

Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn
325 330 335

Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn
340 345 350

Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser
355 360 365

Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu
370 375 380

Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr
385 390 395 400

Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala
 405 410 415
 Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile
 420 425 430
 Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu
 435 440 445
 Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu
 450 455 460
 Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln
 465 470 475 480
 Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser
 485 490 495
 Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser
 500 505 510
 His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu
 515 520 525
 Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val
 530 535 540
 Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln
 545 550 555 560
 Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His
 565 570 575
 Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp
 580 585 590
 Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile
 595 600 605
 Leu Lys Val Leu Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe
 610 615 620
 Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr
 625 630 635 640
 Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu
 645 650 655
 Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp
 660 665 670
 Val Leu Thr Thr Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser
 675 680 685
 Ala Leu Ser Tyr Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys
 690 695 700
 Thr Lys Asn Leu Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly
 705 710 715 720
 Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser
 725 730 735
 Arg Gln Glu Cys Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val
 740 745 750

Glu Asp Ser Lys Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly
 755 760 765
 Thr Thr Leu Trp Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp
 770 775 780
 Lys Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro
 785 790 795 800
 Val Thr Pro Ser Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met
 805 810 815
 Asn Tyr Asp Pro Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp
 820 825 830
 Ile Asn Lys Leu Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys
 835 840 845
 Asn Gln Pro Thr Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu
 850 855 860
 Lys Arg Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu
 865 870 875 880
 Cys Arg Tyr Asp Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys
 885 890 895
 Ser Leu Lys Pro Glu Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys
 900 905 910
 Glu Ile Glu Ile Leu Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr
 915 920 925
 Lys Gly Ile Cys Thr Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met
 930 935 940
 Glu Phe Leu Pro Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys
 945 950 955 960
 Asn Lys Ile Asn Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys
 965 970 975
 Lys Gly Met Asp Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu
 980 985 990
 Ala Ala Arg Asn Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly
 995 1000 1005
 Asp Phe Gly Leu Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr
 1010 1015 1020
 Val Lys Asp Asp Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys
 1025 1030 1035 1040
 Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly
 1045 1050 1055
 Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro
 1060 1065 1070
 Met Ala Leu Phe Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr
 1075 1080 1085
 Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys
 1090 1095 1100

Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp
 1105 1110 1115 1120
 Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly
 1125 1130 1135
 Phe Glu Ala Leu Leu Lys
 1140

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG CCT CTG CGC CAC TGG GGG ATG GCC AGG GGC AGT AAG CCC GTT GGG Met Pro Leu Arg His Trp Gly Met Ala Arg Gly Ser Lys Pro Val Gly 1 5 10 15	48
GAT GGA GCC CAG CCC ATG GCT GCC ATG GGA GGC CTG AAG GTG CTT CTG Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys Val Leu Leu 20 25 30	96
CAC TGG GCT GGT CCA GGC GGC GGG GAG CCC TGG GTC ACT TTC AGT GAG His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr Phe Ser Glu 35 40 45	144
TCA TCG CTG ACA GCT GAG GAA GTC TGC ATC CAC ATT GCA CAT AAA GTT Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val 50 55 60	192
GGT ATC ACT CCT CCT TGC TTC AAT CTC TTT GCC CTC TTC GAT GCT CAG Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln 65 70 75 80	240
GCC CAA GTC TGG TTG CCC CCA AAC CAC ATC CTA GAG ATC CCC AGA GAT Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp 85 90 95	288
GCA AGC CTG ATG CTA TAT TTC CGC ATA AGG TTT TAT TTC CGG AAC TGG Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Arg Asn Trp 100 105 110	336
CAT GGC ATG AAT CCT CGG GAA CCG GCT GTG TAC CGT TGT GGG CCC CCA His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro 115 120 125	384
GGA ACC GAG GCA TCC TCA GAT CAG ACA GCA CAG GGG ATG CAA CTC CTG Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu 130 135 140	432
GAC CCA GCC TCA TTT GAG TAC CTC TTT GAG CAG GGC AAG CAT GAG TTT Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe 145 150 155 160	480
GTG AAT GAC GTG GCA TCA CTG TGG GAG CTG TCG ACC GAG GAG GAG ATC Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile 165 170 175	528

CAC CAC TTT AAG AAT GAG AGC CTG GGC ATG GCC TTT CTG CAC CTC TGT His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys 180 185 190	576
CAC CTC GCT CTC CGC CAT GGC ATC CCC CTG GAG GAG GTG GCC AAG AAG His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys 195 200 205	624
ACC AGC TTC AAG GAC TGC ATC CCG CGC TCC TTC CGC CGG CAT ATC CGG Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg 210 215 220	672
CAG CAC AGC GCC CTG ACC CGG CTG CGC CTT CGG AAC GTC TTC CGC AGG Gln His Ser Ala Leu Thr Arg Leu Arg Leu Asn Val Phe Arg Arg 225 230 235 240	720
TTC CTG CGG GAC TTC CAG CCG GGC CGA CTC TCC CAG CAG ATG GTC ATG Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met 245 250 255	768
GTC AAA TAC CTA GCC ACA CTC GAG CGG CTG GCA CCC CGC TTC GGC ACA Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr 260 265 270	816
GAG CGT GTG CCC GTG TGC CAC CTG AGG CTG CTG GCC CAG GCC GAG GGG Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly 275 280 285	864
GAG CCC TGC TAC ATC CGG GAC AGT GGG GTG GCC CCT ACA GAC CCT GGC Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly 290 295 300	912
CCT GAG TCT GCT GCT GGG CCC CCA ACC CAC GAG GTG CTG GTG ACA GGC Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly 305 310 315 320	960
ACT GGT GGC ATC CAG TGG TGG CCA GTA GAG GAG GAG GTG AAC AAG GAG Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Glu Val Asn Lys Glu 325 330 335	1008
GAG GGT TCT AGT GGC AGC AGT GGC AGG AAC CCC CAA GCC AGC CTG TTT Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe 340 345 350	1056
GGG AAG AAG GCC AAG GCT CAC AAG GCA TTC GGC CAG CCG GCA GAC AGG Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg 355 360 365	1104
CCG CGG GAG CCA CTG TGG GCC TAC TTC TGT GAC TTC CGG GAC ATC ACC Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr 370 375 380	1152
CAC GTG GTG CTG AAA GAG CAC TGT GTC AGC ATC CAC CGG CAG GAC AAC His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn 385 390 395 400	1200
AAG TGC CTG GAG CTG AGC TTG CCT TCC CGG GCT GCG GCG CTG TCC TTC Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe 405 410 415	1248
GTG TCG CTG GTG GAC GGC TAT TTC CGC CTG ACG GCC GAC TCC AGC CAC Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His 420 425 430	1296
TAC CTG TGC CAC GAG GTG GCT CCC CCA CGG CTG GTG ATG AGC ATC CGG Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg 435 440 445	1344

GAT GGG ATC CAC GGA CCC CTG CTG GAG CCA TTT GTG CAG GCC AAG CTG Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu 450 455 460	1392
CGG CCC GAG GAC GGC CTG TAC CTC ATT CAC TGG AGC ACC AGC CAC CCC Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro 465 470 475 480	1440
TAC CGC CTG ATC CTC ACA GTG GCC CAG CGT AGC CAG GCA CCA GAC GGC Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly 485 490 495	1488
ATG CAG AGC TTG CGG CTC CGA AAG TTC CCC ATT GAG CAG CAG GAC GGG Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly 500 505 510	1536
GCC TTC GTG CTG GAG GGC TGG GGC CGG TCC TTC CCC AGC GTT CGG GAA Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu 515 520 525	1584
CTT GGG GCT GCC TTG CAG GGC TGC TTG CTG AGG GCC GGG GAT GAC TGC Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys 530 535 540	1632
TTC TCT CTG CGT CGC TGT TGC CTG CCC CAA CCA GGA GAA ACC TCC AAT Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn 545 550 555 560	1680
CTC ATC ATC ATG CGG GGG GCT CGG GCC AGC CCC AGG ACA CTC AAC CTC Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu 565 570 575	1728
AGC CAG CTC AGC TTC CAC CGG GTT GAC CAG AAG GAG ATC ACC CAG CTG Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu 580 585 590	1776
TCC CAC TTG GGC CAG GGC ACA AGG ACC AAC GTG TAT GAG GGC CGC CTG Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu 595 600 605	1824
CGA GTG GAG GGC AGC GGG GAC CCT GAG GAG GGC AAG ATG GAT GAC GAG Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu 610 615 620	1872
GAC CCC CTC GTG CCT GGC AGG GAC CGT GGG CAG GAG CTA CGA GTG GTG Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val 625 630 635 640	1920
CTC AAA GTG CTG GAC CCT AGT CAC CAT GAC ATC GCC CTG GCC TTC TAC Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr 645 650 655	1968
GAG ACA GCC AGC CTC ATG AGC CAG GTC TCC CAC ACG CAC CTG GCC TTC Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe 660 665 670	2016
GTG CAT GGC GTC TGT GTG CGC GGC CCT GAA AAT AGC ATG GTG ACA GAG Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu 675 680 685	2064
TAC GTG GAG CAC GGA CCC CTG GAT GTG TGG CTG CGG AGG GAG CGG GGC Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly 690 695 700	2112
CAT GTG CCC ATG GCT TGG AAG ATG GTG GTG GCC CAG CAG CTG GCC AGC His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser 705 710 715 720	2160

GCC	CTC	AGC	TAC	CTG	GAG	AAC	AAG	AAC	CTG	GTT	CAT	GGT	AAT	GTG	TGT	2208
Ala	Leu	Ser	Tyr	Leu	Glu	Asn	Lys	Asn	Leu	Val	His	Gly	Asn	Val	Cys	
				725					730					735		
GGC	CGG	AAC	ATC	CTG	CTG	GCC	CGG	CTG	GGG	TTG	GCA	GAG	GGC	ACC	AGC	2256
Gly	Arg	Asn	Ile	Leu	Leu	Ala	Arg	Pro	Gly	Leu	Ala	Glu	Gly	Thr	Ser	
			740					745					750			
CCC	TTC	ATC	AAG	CTG	AGT	GAT	CCT	GGC	GTG	GGC	CTG	GGC	GCC	CTC	TCC	2304
Pro	Phe	Ile	Lys	Leu	Ser	Asp	Pro	Gly	Val	Gly	Leu	Gly	Ala	Leu	Ser	
		755					760					765				
AGG	GAG	GAG	CGG	GTG	GAG	AGG	ATC	CCC	TGG	CTG	GCC	CCC	GAA	TGC	CTA	2352
Arg	Glu	Glu	Arg	Val	Glu	Arg	Ile	Pro	Trp	Leu	Ala	Pro	Glu	Cys	Leu	
	770					775					780					
CCA	GGT	GGG	GCC	AAC	AGC	CTA	AGC	ACC	GCC	ATG	GAC	AAG	TGG	GGG	TTT	2400
Pro	Gly	Gly	Ala	Asn	Ser	Leu	Ser	Thr	Ala	Met	Asp	Lys	Trp	Gly	Phe	
	785				790				795						800	
GGC	GCC	ACC	CTC	CTG	GAG	ATC	TGC	TTT	GAC	GGA	GAG	GCC	CCT	CTG	CAG	2448
Gly	Ala	Thr	Leu	Leu	Glu	Ile	Cys	Phe	Asp	Gly	Glu	Ala	Pro	Leu	Gln	
			805						810					815		
AGC	CGC	AGT	CCC	TCC	GAG	AAG	GAG	CAT	TTC	TAC	CAG	AGG	CAG	CAC	CGG	2496
Ser	Arg	Ser	Pro	Ser	Glu	Lys	Glu	His	Phe	Tyr	Gln	Arg	Gln	His	Arg	
			820					825					830			
CTG	CCC	GAG	CCC	TCC	TGC	CCA	CAG	CTG	GCC	ACA	CTC	ACC	AGC	CAG	TGT	2544
Leu	Pro	Glu	Pro	Ser	Cys	Pro	Gln	Leu	Ala	Thr	Leu	Thr	Ser	Gln	Cys	
		835				840						845				
CTG	ACC	TAT	GAG	CCA	ACC	CAG	AGG	CCA	TCA	TTC	CGC	ACC	ATC	CTG	CGT	2592
Leu	Thr	Tyr	Glu	Pro	Thr	Gln	Arg	Pro	Ser	Phe	Arg	Thr	Ile	Leu	Arg	
	850					855					860					
GAC	CTC	ACC	CGC	GTG	CAG	CCC	CAC	AAT	CTT	GCT	GAC	GTC	TTG	ACT	GTG	2640
Asp	Leu	Thr	Arg	Val	Gln	Pro	His	Asn	Leu	Ala	Asp	Val	Leu	Thr	Val	
	865			870					875						880	
AAC	CGG	GAC	TCA	CCG	GCC	GTC	GGA	CCT	ACT	ACT	TTC	CAC	AAG	CGC	TAT	2688
Asn	Arg	Asp	Ser	Pro	Ala	Val	Gly	Pro	Thr	Thr	Phe	His	Lys	Arg	Tyr	
			885					890						895		
TTG	AAA	AAG	ATC	CGA	GAT	CTG	GGC	GAG	GGT	CAC	TTC	GGC	AAG	GTC	AGC	2736
Leu	Lys	Lys	Ile	Arg	Asp	Leu	Gly	Glu	Gly	His	Phe	Gly	Lys	Val	Ser	
		900					905					910				
TTG	TAC	TGC	TAC	GAT	CCG	ACC	AAC	GAC	GGC	ACT	GGC	GAG	ATG	GTG	GCG	2784
Leu	Tyr	Cys	Tyr	Asp	Pro	Thr	Asn	Asp	Gly	Thr	Gly	Glu	Met	Val	Ala	
		915				920					925					
GTG	AAA	GCC	CTC	AAG	GCA	GAC	TGC	GGC	CCC	CAG	CAC	CGC	TCG	GGC	TGG	2832
Val	Lys	Ala	Leu	Lys	Ala	Asp	Cys	Gly	Pro	Gln	His	Arg	Ser	Gly	Trp	
	930				935					940						
AAG	CAG	GAG	ATT	GAC	ATT	CTG	CGC	ACG	CTC	TAC	CAC	GAG	CAC	ATC	ATC	2880
Lys	Gln	Glu	Ile	Asp	Ile	Leu	Arg	Thr	Leu	Tyr	His	Glu	His	Ile	Ile	
	945			950					955					960		
AAG	TAC	AAG	GGC	TGC	TGC	GAG	GAC	CAA	GGC	GAG	AAG	TCG	CTG	CAG	CTG	2928
Lys	Tyr	Lys	Gly	Cys	Cys	Glu	Asp	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Leu	
			965					970						975		
GTC	ATG	GAG	TAC	GTG	CCC	CTG	GGC	AGC	CTC	CGA	GAC	TAC	CTG	CCC	CGG	2976
Val	Met	Glu	Tyr	Val	Pro	Leu	Gly	Ser	Leu	Arg	Asp	Tyr	Leu	Pro	Arg	
		980					985						990			

CAC AGC ATC GGG CTG GCC CAG CTG CTG CTC TTC GCC CAG CAG ATC TGC His Ser Ile Gly Leu Ala Gln Leu Leu Leu Phe Ala Gln Gln Ile Cys 995 1000 1005	3024
GAG GGC ATG GCC TAT CTG CAC GCG CAC GAC TAC ATC CAC CGA GAC CTA Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu 1010 1015 1020	3072
GCC GCG CGC AAC GTG CTG CTG GAC AAC GAC AGG CTG GTC AAG ATC GGG Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly 1025 1030 1035 1040	3120
GAC TTT GGC CTA GCC AAG GCC GTG CCC GAA GGC CAC GAG TAC TAC CGC Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg 1045 1050 1055	3168
GTG CGC GAG GAT GGG GAC AGC CCC GTG TTC TGG TAT GCC CCA GAG TGC Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys 1060 1065 1070	3216
CTG AAG GAG TAT AAG TTC TAC TAT GCG TCA GAT GTC TGG TCC TTC GGG Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly 1075 1080 1085	3264
GTG ACC CTG TAT GAG CTG CTG ACG CAC TGT GAC TCC AGC CAG AGC CCC Val Thr Leu Tyr Glu Leu Thr His Cys Asp Ser Ser Gln Ser Pro 1090 1095 1100	3312
CCC ACG AAA TTC CTT GAG CTC ATA GGC ATT GCT CAG GGT CAG ATG ACA Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr 1105 1110 1115 1120	3360
GTT CTG AGA CTC ACT GAG TTG CTG GAA CGA GGG GAG AGG CTG CCA CGG Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg 1125 1130 1135	3408
CCC GAC AAA TGT CCC TGT GAG GTC TAT CAT CTC ATG AAG AAC TGC TGG Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp 1140 1145 1150	3456
GAG ACA GAG GCG TCC TTT CGC CCA ACC TTC GAG AAC CTC ATA CCC ATT Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile 1155 1160 1165	3504
CTG AAG ACA GTC CAT GAG AAG TAC CAA GGC CAG GCC CCT TCA GTG TTC Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe 1170 1175 1180	3552
AGC GTG TGC Ser Val Cys 1185	3561

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Leu Arg His Trp Gly Met Ala Arg Gly Ser Lys Pro Val Gly
1 5 10 15

Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys Val Leu Leu
 20 25 30
 His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr Phe Ser Glu
 35 40 45
 Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val
 50 55 60
 Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln
 65 70 75 80
 Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp
 85 90 95
 Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Arg Asn Trp
 100 105 110
 His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro
 115 120 125
 Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu
 130 135 140
 Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe
 145 150 155 160
 Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile
 165 170 175
 His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys
 180 185 190
 His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys
 195 200 205
 Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg
 210 215 220
 Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val Phe Arg Arg
 225 230 235 240
 Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met
 245 250 255
 Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr
 260 265 270
 Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly
 275 280 285
 Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly
 290 295 300
 Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly
 305 310 315 320
 Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Glu Val Asn Lys Glu
 325 330 335
 Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe
 340 345 350
 Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg
 355 360 365

Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr
370 375 380

His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn
385 390 395 400

Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe
405 410 415

Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His
420 425 430

Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg
435 440 445

Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu
450 455 460

Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro
465 470 475 480

Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly
485 490 495

Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly
500 505 510

Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu
515 520 525

Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys
530 535 540

Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn
545 550 555 560

Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu
565 570 575

Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu
580 585 590

Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu
595 600 605

Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu
610 615 620

Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val
625 630 635 640

Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr
645 650 655

Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe
660 665 670

Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu
675 680 685

Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly
690 695 700

His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser
705 710 715 720

Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly Asn Val Cys
725 730 735

Gly Arg Asn Ile Leu Leu Ala Arg Leu Gly Leu Ala Glu Gly Thr Ser
740 745 750

Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly Ala Leu Ser
755 760 765

Arg Glu Glu Arg Val Glu Arg Ile Pro Trp Leu Ala Pro Glu Cys Leu
770 775 780

Pro Gly Gly Ala Asn Ser Leu Ser Thr Ala Met Asp Lys Trp Gly Phe
785 790 795 800

Gly Ala Thr Leu Leu Glu Ile Cys Phe Asp Gly Glu Ala Pro Leu Gln
805 810 815

Ser Arg Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg
820 825 830

Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr Ser Gln Cys
835 840 845

Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr Ile Leu Arg
850 855 860

Asp Leu Thr Arg Val Gln Pro His Asn Leu Ala Asp Val Leu Thr Val
865 870 875 880

Asn Arg Asp Ser Pro Ala Val Gly Pro Thr Thr Phe His Lys Arg Tyr
885 890 895

Leu Lys Lys Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Ser
900 905 910

Leu Tyr Cys Tyr Asp Pro Thr Asn Asp Gly Thr Gly Glu Met Val Ala
915 920 925

Val Lys Ala Leu Lys Ala Asp Cys Gly Pro Gln His Arg Ser Gly Trp
930 935 940

Lys Gln Glu Ile Asp Ile Leu Arg Thr Leu Tyr His Glu His Ile Ile
945 950 955 960

Lys Tyr Lys Gly Cys Cys Glu Asp Gln Gly Glu Lys Ser Leu Gln Leu
965 970 975

Val Met Glu Tyr Val Pro Leu Gly Ser Leu Arg Asp Tyr Leu Pro Arg
980 985 990

His Ser Ile Gly Leu Ala Gln Leu Leu Phe Ala Gln Gln Ile Cys
995 1000 1005

Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu
1010 1015 1020

Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly
1025 1030 1035 1040

Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg
1045 1050 1055

Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys
1060 1065 1070

Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly
 1075 1080 1085
 Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro
 1090 1095 1100
 Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr
 1105 1110 1115 1120
 Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg
 1125 1130 1135
 Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp
 1140 1145 1150
 Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile
 1155 1160 1165
 Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe
 1170 1175 1180
 Ser Val Cys
 1185

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Tyr Leu Asn Ile Lys Glu Asp Cys Asn Ala Met Ala Phe Cys
 1 5 10 15
 Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn Leu Glu Ala Pro
 20 25 30
 Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp Arg Glu Pro Leu
 35 40 45
 Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu Cys Ile Arg Ala
 50 55 60
 Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn Leu Phe Ala Leu
 65 70 75 80
 Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn Arg Thr Ile Thr
 85 90 95
 Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg Met Arg Phe Tyr
 100 105 110
 Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln Ser Val Trp Arg
 115 120 125
 His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys Lys Lys Ile Pro
 130 135 140
 Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu Tyr Leu Phe Ala
 145 150 155 160

Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro Ile Arg Asp Pro
165 170 175

Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu Cys Leu Gly Met
180 185 190

Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys Lys Met Gln Leu
195 200 205

Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr Ile Pro Glu Thr
210 215 220

Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr Arg Met Arg Ile
225 230 235 240

Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn Asn Lys Thr Ile
245 250 255

Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val Lys Tyr Leu Ala
260 265 270

Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu Ile Phe Glu Thr
275 280 285

Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn Trp Phe His Ser
290 295 300

Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met Val Thr Gly Asn
305 310 315 320

Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val Val Ser Val Glu Lys
325 330 335

Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn Lys Asp Lys Lys
340 345 350

Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn Asn Phe Ser Phe
355 360 365

Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser Val Val Ser Ile
370 375 380

Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu Ser Ser His Glu
385 390 395 400

Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr
405 410 415

Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala Pro Pro Leu Ile
420 425 430

Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile Cys Thr Glu Tyr
435 440 445

Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu Gly Met Tyr Val
450 455 460

Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu Met Thr Val Thr
465 470 475 480

Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln Lys Gln Phe Lys
485 490 495

Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser Leu His Gly Ser
500 505 510

Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser His Leu Lys Lys
515 520 525

Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu Lys Arg Cys Cys
530 535 540

Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val Ala Thr Lys Lys
545 550 555 560

Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln Leu Ser Phe Asp
565 570 575

Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His Leu Gly Arg Gly
580 585 590

Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp Tyr Lys Asp Asp
595 600 605

Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile Leu Lys Val Leu
610 615 620

Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe Glu Ala Ala Ser
625 630 635 640

Met Met Arg Gln Val Ser His Lys His Ile Val Tyr Leu Tyr Gly Val
645 650 655

Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu Phe Val Glu Gly
660 665 670

Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp Val Leu Thr Thr
675 680 685

Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser Ala Leu Ser Tyr
690 695 700

Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys Thr Lys Asn Leu
705 710 715 720

Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly Pro Phe Ile Lys
725 730 735

Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser Arg Gln Glu Cys
740 745 750

Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val Glu Asp Ser Lys
755 760 765

Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly Thr Thr Leu Trp
770 775 780

Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp Lys Thr Leu Ile
785 790 795 800

Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val Thr Pro Ser
805 810 815

Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met Asn Tyr Asp Pro
820 825 830

Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp Ile Asn Lys Leu
835 840 845

Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys Asn Gln Pro Thr
850 855 860

Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu Lys Arg Ile Arg
865 870 875 880

Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu Cys Arg Tyr Asp
885 890 895

Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys Ser Leu Lys Pro
900 905 910

Glu Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys Glu Ile Glu Ile
915 920 925

Leu Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr Lys Gly Ile Cys
930 935 940

Thr Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met Glu Phe Leu Pro
945 950 955 960

Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys Asn Lys Ile Asn
965 970 975

Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys Lys Gly Met Asp
980 985 990

Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu Ala Ala Arg Asn
995 1000 1005

Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly Asp Phe Gly Leu
1010 1015 1020

Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp
1025 1030 1035 1040

Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys Leu Met Gln Ser
1045 1050 1055

Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly Val Thr Leu His
1060 1065 1070

Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro Met Ala Leu Phe
1075 1080 1085

Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr Val Thr Arg Leu
1090 1095 1100

Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys Pro Pro Asn Cys
1105 1110 1115 1120

Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp Glu Phe Gln Pro
1125 1130 1135

Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly Phe Glu Ala Leu
1140 1145 1150

Leu Lys

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Lys Leu Leu Pro Leu Asp Lys Asp Tyr Tyr Val Val Arg
1 5 10 15

Glu Pro Gly
18